In recent studies, diverse patterns of cytoplasmic incompatibility (CI) induced by Wolbachia in Tetranychus urticae have been reported in two spotted spider mites (Tetranychus urticae). The mechanism of CI consists of two steps: modification of sperm of infected males and rescuing (resc) of these recombinants by Wolbachia in the egg, which results in either female embryonic mortality (FM), male development (MD) or no CI (O'Neill et al., 1998). Our study reports that Wolbachia highly prevailed in T. urticae infecting all collected mite populations from various crops in 14 different commercial greenhouses in Korea, which included two Wolbachia strains expressing different phenotypic effects on hosts. Analyses for 550-bp portion of Wolbachia wsp gene sequences categorized all Wolbachia strains from the collected mite populations into two groups (A and B) based on analyses of partial sequences of wsp gene.

**RESULTS**

Detection of Wolbachia and Analyses of Partial Sequences of wsp gene

**ABSTRACT**

Among the 14 mite populations were established from original crosses. PCR assay is conducted for total 39 clones from 15 individual mites that discriminated by three diagnostic nucleotides. Various mating experiments with the mite populations from each group showed CI patterns exactly followed with the grouping: no CI (mod-resc+) for group A and mixed pattern of FM and MD (mod+resc+) for group B. Evolutionary implications were discussed for phenotypic effects in association with genetic and host plant variations.

**INTRODUCTION**

Most previous studies on CI in infected males or when infected females are fertilized by males harboring a Wolbachia strain have been conducted in insects, mites, nematodes and crustaceans (Stouthamer et al., 1998). The most common effects of Wolbachia on insects are female mortality (FM), male development (MD) or both (Stouthamer et al., 1998). In Tetranychus urticae, CI is caused by two Wolbachia strains, one of which is male cytoplasmic incompatibility (MC) and the other female cytoplasmic incompatibility (FC). The MC occurs when unmated females are fertilized by infected males or when infected females are fertilized by males harboring a different Wolbachia strain. More specifically, mechanism of CI has been known to involve two steps (Wenm, 1999): modification (mod) of sperm of infected males and rescuing (resc) of these recombinants in the egg. The infection phenotype can be detected either male or female-resistant (mod-resc) or female-resistant (mod+resc) whether infected Wolbachia is capable of both modifying and rescuing or not. The phenotype of Wolbachia depends on the combination of these two mechanisms. Most previous studies on CI in Tetranychus urticae dealt with the modification, yet little known for the rescuing.

**MATERIALS AND METHODS**

**Methods**

-The infection phenotype can be detected either male or female-resistant (mod-resc) or female-resistant (mod+resc) whether infected Wolbachia is capable of both modifying and rescuing or not. The phenotype of Wolbachia depends on the combination of these two mechanisms. Most previous studies on CI in Tetranychus urticae dealt with the modification, yet little known for the rescuing.

-Intra- and inter-population crossing experiments were conducted between four infected populations (GC, SC, SW and JE) and cured populations (GCt, SCt, JEt and JEt). Fourteen sets of crosses (male X female) were established for total 39 clones from 15 individual mites that discriminated by three diagnostic nucleotides. Various mating experiments with the mite populations from each group showed CI patterns exactly followed with the grouping: no CI (mod-resc+) for group A and mixed pattern of FM and MD (mod+resc+) for group B. Evolutionary implications were discussed for phenotypic effects in association with genetic and host plant variations.

**CONCLUSION**

**REFERENCES**

**Fig. 1.** A phylogenetic tree based on wsp gene sequences from each mite population (GC, SC, SW and JE). The tree is based on the neighbor-joining method with Kimura's 2-parameter model. The tree was rooted to Wolbachia strain WspB of Culex pipiens. (A) Lane 1: IC, 2: SW, 3: JC, 4: BY, 5: DJ, 6: JJ, 7: JE, 8: JEt, 9: SCt, 10: SC, 11: SW, 12: SP, 13: SJ, 14: JEt, 15: GNt, 16: GN, 17: JEt. (B) Lane 1: GC, 2: SC, 3: SW, 4: JE, 5: GJs, 6: SCt, 7: SC, 8: SW, 9: JEt, 10: GNt, 11: GN. *(Correspondence should be addressed. E-mail: kjcho@korea.ac.kr Tel: +82-2-3290-3064)

**Table 1.** Host plants information of field-collected Tetranychus urticae populations from group A and B categorized by analyses of partial sequences of wsp gene.

**Table 2.** Reproductive parameters in crosses (female x male) between infected and cured populations of Tetranychus urticae.

**Table 3.** Reproductive parameters in crosses (female x male) within group B (mod+resc+).

**Table 4.** Reproductive parameters in crosses (female x male) between Wolbachia strains within Tetranychus urticae.

**Table 5.** A phylogenetic tree based on wsp gene sequences from each mite population (GC, SC, SW and JE). The tree is based on the neighbor-joining method with Kimura's 2-parameter model. The tree was rooted to Wolbachia strain WspB of Culex pipiens. (A) Lane 1: IC, 2: SW, 3: JC, 4: BY, 5: DJ, 6: JJ, 7: JE, 8: JEt, 9: SCt, 10: SC, 11: SW, 12: SP, 13: SJ, 14: JEt, 15: GNt, 16: GN, 17: JEt. (B) Lane 1: GC, 2: SC, 3: SW, 4: JE, 5: GJs, 6: SCt, 7: SC, 8: SW, 9: JEt, 10: GNt, 11: GN. *(Correspondence should be addressed. E-mail: kjcho@korea.ac.kr Tel: +82-2-3290-3064)

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**Fig. 5.** A phylogenetic tree based on wsp gene sequences from each mite population (GC, SC, SW and JE). The tree is based on the neighbor-joining method with Kimura's 2-parameter model. The tree was rooted to Wolbachia strain WspB of Culex pipiens. (A) Lane 1: IC, 2: SW, 3: JC, 4: BY, 5: DJ, 6: JJ, 7: JE, 8: JEt, 9: SCt, 10: SC, 11: SW, 12: SP, 13: SJ, 14: JEt, 15: GNt, 16: GN, 17: JEt. (B) Lane 1: GC, 2: SC, 3: SW, 4: JE, 5: GJs, 6: SCt, 7: SC, 8: SW, 9: JEt, 10: GNt, 11: GN. *(Correspondence should be addressed. E-mail: kjcho@korea.ac.kr Tel: +82-2-3290-3064)

**Fig. 6.** A phylogenetic tree based on wsp gene sequences from each mite population (GC, SC, SW and JE). The tree is based on the neighbor-joining method with Kimura's 2-parameter model. The tree was rooted to Wolbachia strain WspB of Culex pipiens. (A) Lane 1: IC, 2: SW, 3: JC, 4: BY, 5: DJ, 6: JJ, 7: JE, 8: JEt, 9: SCt, 10: SC, 11: SW, 12: SP, 13: SJ, 14: JEt, 15: GNt, 16: GN, 17: JEt. (B) Lane 1: GC, 2: SC, 3: SW, 4: JE, 5: GJs, 6: SCt, 7: SC, 8: SW, 9: JEt, 10: GNt, 11: GN. *(Correspondence should be addressed. E-mail: kjcho@korea.ac.kr Tel: +82-2-3290-3064)